

SEQLIST.TXT
SEQUENCE LISTING

<110> Novartis AG
McCullough, Karen
Ide, Susan
Lavedan, Christian

<120> USE OF GENETIC POLYMORPHISMS THAT
ASSOCIATE WITH EFFICACY OF TREATMENT OF INFLAMMATORY DISEASE

<130> DV/4-33389A

<150> 60/508,971
<151> 2003-10-06

<160> 22

<170> FastSEQ for windows Version 4.0

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<212> DNA
<213> Homo sapiens

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<222> (1)...(53)
<223> TNF locus variant (T at position -1031)

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<222> (23)...(0)
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<220>
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<222> (1)...(53)
<223> TNF locus variant (C at position -1031)

<221> variation
<222> (23)...(0)
<223> C

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<212> DNA
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<222> (1)...(48)
<223> LTA locus variant (C)

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SEQLIST.TXT

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gtgagcagca ggtttgaggc tgctgtgggc aagatgcatc ttgggggtg 48

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<222> (1)...(48)
<223> LTA locus variant (A; ASN60THR)

<221> variation
<222> (20)...(0)
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<223> CCR2 locus variant (G)

<221> variation
<222> (10)...(0)
<223> G

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<210> 6
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<213> Homo sapiens

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<222> (1)...(50)
<223> CCR2 locus variant (A; VAL64ILE)

<221> variation
<222> (10)...(0)
<223> A

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<210> 7
<211> 702
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(702)
<223> Tumor necrosis factor alpha (TNFalpha) mRNA
coding region

<400> 7
atg agc act gaa agc atg atc cgg gac gtg gag ctg gcc gag gag gcg 48

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SEQLIST.TXT

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Leu	Pro	Lys	Lys 20	Thr	Gly	Gly	Pro	Gln 25	Gly	Ser	Arg	Arg	Cys 30	Leu	Phe	
ctc	agc	ctc	ttc	tcc	ttc	ctg	atc	gtg	gca	ggc	gcc	acc	acg	ctc	ttc	144
Leu	Ser	Leu 35	Phe	Ser	Phe	Leu	Ile 40	Val	Ala	Gly	Ala	Thr 45	Thr	Leu	Phe	
tgc	ctg	ctg	cac	ttt	gga	gtg	atc	ggc	ccc	cag	agg	gaa	gag	ttc	ccc	192
Cys	Leu 50	Leu	His	Phe	Gly	Val 55	Ile	Gly	Pro	Gln	Arg 60	Glu	Glu	Phe	Pro	
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Arg 65	Asp	Leu	Ser	Leu	Ile 70	Ser	Pro	Leu	Ala	Gln 75	Ala	Val	Arg	Ser	Ser 80	
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Gln	Ala	Glu	Gly 100	Gln	Leu	Gln	Trp	Leu 105	Asn	Arg	Arg	Ala	Asn 110	Ala	Leu	
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Leu	Ala	Asn 115	Gly	Val	Glu	Leu	Arg 120	Asp	Asn	Gln	Leu	Val 125	Val	Pro	Ser	
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Glu	Gly 130	Leu	Tyr	Leu	Ile	Tyr 135	Ser	Gln	Val	Leu	Phe 140	Lys	Gly	Gln	Gly	
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Cys 145	Pro	Ser	Thr	His	Val 150	Leu	Leu	Thr	His	Thr 155	Ile	Ser	Arg	Ile	Ala 160	
gtc	tcc	tac	cag	acc	aag	gtc	aac	ctc	ctc	tct	gcc	atc	aag	agc	ccc	528
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Cys	Gln	Arg	Glu 180	Thr	Pro	Glu	Gly	Ala 185	Glu	Ala	Lys	Pro	Trp 190	Tyr	Glu	
ccc	atc	tat	ctg	gga	ggg	gtc	ttc	cag	ctg	gag	aag	ggt	gac	cga	ctc	624
Pro	Ile	Tyr 195	Leu	Gly	Gly	Val	Phe 200	Gln	Leu	Glu	Lys	Gly 205	Asp	Arg	Leu	
agc	gct	gag	atc	aat	cgg	ccc	gac	tat	ctc	gac	ttt	gcc	gag	tct	ggg	672
Ser	Ala 210	Glu	Ile	Asn	Arg	Pro 215	Asp	Tyr	Leu	Asp	Phe 220	Ala	Glu	Ser	Gly	
cag	gtc	tac	ttt	ggg	atc	att	gcc	ctg	tga							702
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225																

<210> 8

<211> 233

<212> PRT

<213> Homo sapiens

<400> 8

Met 1	Ser	Thr	Glu	Ser 5	Met	Ile	Arg	Asp	Val 10	Glu	Leu	Ala	Glu	Glu 15	Ala
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SEQLIST.TXT

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Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
                20                25                30
Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
                35                40                45
Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
                50                55                60
Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
65                70                75                80
Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
                85                90                95
Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
                100                105                110
Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
                115                120                125
Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
130                135                140
Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
145                150                155                160
Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
                165                170                175
Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
                180                185                190
Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
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Gln Val Tyr Phe Gly Ile Ile Ala Leu
225                230

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<210> 9
 <211> 1793
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (74)...(1201)
 <223> beta-actin expression (ACTB) mRNA coding region

```

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                Met Asp Asp Asp Ile Ala Ala Leu Val Val Asp Asn
                1                5                10

ggc tcc ggc atg tgc aag gcc ggc ttc gcg ggc gac gat gcc ccc cgg 157
Gly Ser Gly Met Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg
                15                20                25

gcc gtc ttc ccc tcc atc gtg ggg cgc ccc agg cac cag ggc gtg atg 205
Ala Val Phe Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met
                30                35                40

gtg ggc atg ggt cag aag gat tcc tat gtg ggc gac gag gcc cag agc 253
Val Gly Met Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser
45                50                55                60

aag aga ggc atc ctc acc ctg aag tac ccc atc gag cac ggc atc gtc 301
Lys Arg Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val
                65                70                75

acc aac tgg gac gac atg gag aaa atc tgg cac cac acc ttc tac aat 349
Thr Asn Trp Asp Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn
                80                85                90

gag ctg cgt gtg gct ccc gag gag cac ccc gtg ctg ctg acc gag gcc 397
Glu Leu Arg Val Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala

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SEQLIST.TXT

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gag Glu 125	acc Thr	ttc Phe	aac Asn	acc Thr	cca Pro 130	gcc Ala	atg Met	tac Tyr	gtt Val	gct Ala 135	atc Ile	cag Gln	gct Ala	gtg Val	cta Leu 140	493
tcc Ser	ctg Leu	tac Tyr	gcc Ala	tct Ser 145	ggc Gly	cgt Arg	acc Thr	act Thr	ggc Gly 150	atc Ile	gtg Val	atg Met	gac Asp	tcc Ser 155	ggt Gly	541
gac Asp	ggg Gly	gtc Val	acc Thr 160	cac His	act Thr	gtg Val	ccc Pro	atc Ile 165	tac Tyr	gag Glu	ggg Gly	tat Tyr	gcc Ala 170	ctc Leu	ccc Pro	589
cat His	gcc Ala 175	atc Ile	ctg Leu	cgt Arg	ctg Leu	gac Asp	ctg Leu 180	gct Ala	ggc Gly	cgg Arg	gac Asp	ctg Leu 185	act Thr	gac Asp	tac Tyr	637
ctc Leu	atg Met 190	aag Lys	atc Ile	ctc Leu	acc Thr	gag Glu 195	cgc Arg	ggc Gly	tac Tyr	agc Ser	ttc Phe 200	acc Thr	acc Thr	acg Thr	gcc Ala	685
gag Glu 205	cgg Arg	gaa Glu	atc Ile	gtg Val	cgt Arg 210	gac Asp	att Ile	aag Lys	gag Glu	aag Lys 215	ctg Leu	tgc Cys	tac Tyr	gtc Val	gcc Ala 220	733
ctg Leu	gac Asp	ttc Phe	gag Glu	caa Gln 225	gag Glu	atg Met	gcc Ala	acg Thr	gct Ala 230	gct Ala	tcc Ser	agc Ser	tcc Ser	tcc Ser 235	ctg Leu	781
gag Glu	aag Lys	agc Ser	tac Tyr 240	gag Glu	ctg Leu	cct Pro	gac Asp	ggc Gly 245	cag Gln	gtc Val	atc Ile	acc Thr	att Ile 250	ggc Gly	aat Asn	829
gag Glu	cgg Arg	ttc Phe 255	cgc Arg	tgc Cys	cct Pro	gag Glu	gca Ala 260	ctc Leu	ttc Phe	cag Gln	cct Pro	tcc Ser 265	ttc Phe	ctg Leu	ggc Gly	877
atg Met 270	gag Glu	tcc Ser	tgt Cys	ggc Gly	atc Ile	cac His 275	gaa Glu	act Thr	acc Thr	ttc Phe	aac Asn 280	tcc Ser	atc Ile	atg Met	aag Lys	925
tgt Cys 285	gac Asp	gtg Val	gac Asp	atc Ile	cgc Arg 290	aaa Lys	gac Asp	ctg Leu	tac Tyr	gcc Ala 295	aac Asn	aca Thr	gtg Val	ctg Leu	tct Ser 300	973
ggc Gly	ggc Gly	acc Thr	acc Thr	atg Met 305	tac Tyr	cct Pro	ggc Gly	att Ile	gcc Ala 310	gac Asp	agg Arg	atg Met	cag Gln	aag Lys 315	gag Glu	1021
atc Ile	act Thr	gcc Ala 320	ctg Leu	gca Ala	ccc Pro	agc Ser	aca Thr	atg Met 325	aag Lys	atc Ile	aag Lys	atc Ile	att Ile 330	gct Ala	cct Pro	1069
cct Pro	gag Glu 335	cgc Arg	aag Lys	tac Tyr	tcc Ser	gtg Val	tgg Trp 340	atc Ile	ggc Gly	ggc Gly	tcc Ser	atc Ile 345	ctg Leu	gcc Ala	tcg Ser	1117
ctg Leu 350	tcc Ser	acc Thr	ttc Phe	cag Gln	cag Gln	atg Met 355	tgg Trp	atc Ile	agc Ser	aag Lys	cag Gln 360	gag Glu	tat Tyr	gac Asp	gag Glu	1165
tcc Ser	ggc Gly	ccc Pro	tcc Ser	atc Ile	gtc Val	cac His	cgc Arg	aaa Lys	tgc Cys	ttc Phe	tag *	gcggactatg				1211

SEQLIST.TXT

365

370

375

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ttgtttttatt ttgaatgatg agccttcgtg ccccccttc cccctttttg tcccccaact 1691
tgagatgtat gaaggctttt ggtctccctg ggagtgggtg gaggcagcca gggcttacct 1751
gtacactgac ttgagaccag ttgaataaaa gtgcacacct ta 1793

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<210> 10

<211> 2242

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (51)...(991)

<223> chemokine (C C motif) receptor 2 (CCR2) mRNA
coding region

<400> 10

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                                     1

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```

tcc aca tct cgt tct cgg ttt atc aga aat acc aac gag agc ggt gaa 104
Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser Gly Glu
                    5                      10                      15

```

```

gaa gtc acc acc ttt ttt gat tat gat tac ggt gct ccc tgt cat aaa 152
Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys His Lys
                20                      25                      30

```

```

ttt gac gtg aag caa att ggg gcc caa ctc ctg cct ccg ctc tac tcg 200
Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser
                35                      40                      45                      50

```

```

ctg gtg ttc atc ttt ggt ttt gtg ggc aac atg ctg gtc gtc ctc atc 248
Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val Leu Ile
                    55                      60                      65

```

```

tta ata aac tgc aaa aag ctg aag tgc ttg act gac att tac ctg ctc 296
Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr Leu Leu
                    70                      75                      80

```

```

aac ctg gcc atc tct gat ctg ctt ttt ctt att act ctc cca ttg tgg 344
Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro Leu Trp
                    85                      90                      95

```

```

gct cac tct gct gca aat gag tgg gtc ttt ggg aat gca atg tgc aaa 392
Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met Cys Lys
                100                      105                      110

```

```

tta ttc aca ggg ctg tat cac atc ggt tat ttt ggc gga atc ttc ttc 440
Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile Phe Phe
                115                      120                      125                      130

```

```

atc atc ctc ctg aca atc gat aga tac ctg gct att gtc cat gct gtg 488
Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val
                    135                      140                      145

```

```

ttt gct tta aaa gcc agg acg gtc acc ttt ggg gtg gtg aca agt gtg 536
Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val
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SEQLIST.TXT

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165 170 175

act aaa tgc cag aaa gaa gat tct gtt tat gtc tgt ggc cct tat ttt 632
Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro Tyr Phe
180 185 190

cca cga gga tgg aat aat ttc cac aca ata atg agg aac att ttg ggg 680
Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile Leu Gly
195 200 205 210

ctg gtc ctg ccg ctg ctc atc atg gtc atc tgc tac tcg gga atc ctg 728
Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly Ile Leu
215 220 225

aaa acc ctg ctt cgg tgt cga aac gag aag aag agg cat agg gca gtg 776
Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val
230 235 240

aga gtc atc ttc acc atc atg att gtt tac ttt ctc ttc tgg act ccc 824
Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Thr Pro
245 250 255

tat aac att gtc att ctc ctg aac acc ttc cag gaa ttc ttc ggc ctg 872
Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu
260 265 270

agt aac tgt gaa agc acc agt caa ctg gac caa gcc acg cag gtg aca 920
Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln Val Thr
275 280 285 290

gag act ctt ggg atg act cac tgc tgc atc aat ccc atc atc tat gcc 968
Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala
295 300 305

ttc gtt ggg gag aag ttc aga ag cctttttcac atagctcttg gctgtaggat 1021
Phe Val Gly Glu Lys Phe Arg
310

tgccccactc caaaaaccag tgtgtggagg tccaggagtg agaccaggaa agaatgtgaa 1081
agtgactaca caaggactcc tcgatggctg tggaaaagga aagtcaattg gcagagcccc 1141
tgaagccagt cttcaggaca aagaaggagc ctgagacagc aaatgacaga tctctgcttt 1201
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<210> 11
<211> 618
<212> DNA
<213> Homo sapiens

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SEQLIST.TXT

<220>

<221> CDS

<222> (1)...(618)

<223> Lymphotoxin alpha (LTA) mRNA coding region

<400> 11

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Met	Thr	Pro	Pro	Glu	Arg	Leu	Phe	Leu	Pro	Arg	Val	Cys	Gly	Thr	Thr	
1				5					10					15		
cta	cac	ctc	ctc	ctt	ctg	ggg	ctg	ctg	ctg	gtt	ctg	ctg	cct	ggg	gcc	96
Leu	His	Leu	Leu	Leu	Leu	Gly	Leu	Leu	Leu	Val	Leu	Leu	Pro	Gly	Ala	
			20				25						30			
cag	ggg	ctc	cct	ggg	gtt	ggc	ctc	aca	cct	tca	gct	gcc	cag	act	gcc	144
Gln	Gly	Leu	Pro	Gly	Val	Gly	Leu	Thr	Pro	Ser	Ala	Ala	Gln	Thr	Ala	
		35					40					45				
cgt	cag	cac	ccc	aag	atg	cat	ctt	gcc	cac	agc	acc	ctc	aaa	cct	gct	192
Arg	Gln	His	Pro	Lys	Met	His	Leu	Ala	His	Ser	Thr	Leu	Lys	Pro	Ala	
	50					55					60					
gct	cac	ctc	att	gga	gac	ccc	agc	aag	cag	aac	tca	ctg	ctc	tgg	aga	240
Ala	His	Leu	Ile	Gly	Asp	Pro	Ser	Lys	Gln	Asn	Ser	Leu	Leu	Trp	Arg	
65				70					75						80	
gca	aac	acg	gac	cgt	gcc	ttc	ctc	cag	gat	ggg	ttc	tcc	ttg	agc	aac	288
Ala	Asn	Thr	Asp	Arg	Ala	Phe	Leu	Gln	Asp	Gly	Phe	Ser	Leu	Ser	Asn	
				85					90					95		
aat	tct	ctc	ctg	gtc	ccc	acc	agt	ggc	atc	tac	ttc	gtc	tac	tcc	cag	336
Asn	Ser	Leu	Leu	Val	Pro	Thr	Ser	Gly	Ile	Tyr	Phe	Val	Tyr	Ser	Gln	
			100					105					110			
gtg	gtc	ttc	tct	ggg	aaa	gcc	tac	tct	ccc	aag	gcc	acc	tcc	tcc	cca	384
Val	Val	Phe	Ser	Gly	Lys	Ala	Tyr	Ser	Pro	Lys	Ala	Thr	Ser	Ser	Pro	
		115					120					125				
ctc	tac	ctg	gcc	cat	gag	gtc	cag	ctc	ttc	tcc	tcc	cag	tac	ccc	ttc	432
Leu	Tyr	Leu	Ala	His	Glu	Val	Gln	Leu	Phe	Ser	Ser	Gln	Tyr	Pro	Phe	
	130					135					140					
cat	gtg	cct	ctc	ctc	agc	tcc	cag	aag	atg	gtg	tat	cca	ggg	ctg	cag	480
His	Val	Pro	Leu	Leu	Ser	Ser	Gln	Lys	Met	Val	Tyr	Pro	Gly	Leu	Gln	
145					150				155					160		
gaa	ccc	tgg	ctg	cac	tcg	atg	tac	cac	ggg	gct	gcg	ttc	cag	ctc	acc	528
Glu	Pro	Trp	Leu	His	Ser	Met	Tyr	His	Gly	Ala	Ala	Phe	Gln	Leu	Thr	
				165					170					175		
cag	gga	gac	cag	cta	tcc	acc	cac	aca	gat	ggc	atc	ccc	cac	cta	gtc	576
Gln	Gly	Asp	Gln	Leu	Ser	Thr	His	Thr	Asp	Gly	Ile	Pro	His	Leu	Val	
			180					185					190			
ctc	agc	cct	agt	act	gtc	ttc	ttt	gga	gcc	ttc	gct	ctg	tag			618
Leu	Ser	Pro	Ser	Thr	Val	Phe	Phe	Gly	Ala	Phe	Ala	Leu	*			
		195				200						205				

<210> 12

<211> 894

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (9)...(743)

SEQLIST.TXT

<223> Lymphotoxin beta (LTB) mRNA coding region

<400> 12

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cagctctca  atg ggg gca ctg ggg ctg gag ggc agg ggt ggg agg ctc cag  50
      Met  Gly Ala Leu  Gly Leu Glu Gly Arg Gly Gly Arg Leu Gln
        1          5          10

ggg agg ggt tcc ctc ctg cta gct gtg gca gga gcc act tct ctg gtg  98
Gly Arg Gly Ser Leu Leu Leu Ala Val Ala Gly Ala Thr Ser Leu Val
  15          20          25          30

acc ttg ttg ctg gcg gtg cct atc act gtc ctg gct gtg ctg gcc tta  146
Thr Leu Leu Leu Ala Val Pro Ile Thr Val Leu Ala Val Leu Ala Leu
          35          40          45

gtg ccc cag gat cag gga gga ctg gta acg gag acg gcc gac ccc ggg  194
Val Pro Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala Asp Pro Gly
          50          55          60

gca cag gcc cag caa gga ctg ggg ttt cag aag ctg cca gag gag gag  242
Ala Gln Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro Glu Glu Glu
          65          70          75

cca gaa aca gat ctc agc ccc ggg ctc cca gct gcc cac ctc ata ggc  290
Pro Glu Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His Leu Ile Gly
          80          85          90

gct ccg ctg aag ggg cag ggg cta ggc tgg gag acg acg aag gaa cag  338
Ala Pro Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln
          95          100          105          110

gcg ttt ctg acg agc ggg acg cag ttc tcg gac gcc gag ggg ctg gcg  386
Ala Phe Leu Thr Ser Gly Thr Gln Phe Ser Ser Asp Ala Glu Gly Leu Ala
          115          120          125

ctc ccg cag gac ggc ctc tat tac ctc tac tgt ctc gtc ggc tac cgg  434
Leu Pro Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg
          130          135          140

ggc cgg gcg ccc cct ggc ggc ggg gac ccc cag ggc cgc tcg gtc acg  482
Gly Arg Ala Pro Pro Gly Gly Gly Asp Pro Gln Gly Arg Ser Val Thr
          145          150          155

ctg cgc agc tct ctg tac cgg gcg ggg ggc gcc tac ggg ccg ggc act  530
Leu Arg Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr
          160          165          170

ccc gag ctg ctg ctc gag ggc gcc gag acg gtg act cca gtg ctg gac  578
Pro Glu Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp
          175          180          185          190

ccg gcc agg aga caa ggg tac ggg cct ctc tgg tac acg agc gtg ggg  626
Pro Ala Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly
          195          200          205

ttc ggc ggc ctg gtg cag ctc cgg agg ggc gag agg gtg tac gtc aac  674
Phe Gly Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn
          210          215          220

atc agt cac ccc gat atg gtg gac ttc gcg aga ggg aag acc ttc ttt  722
Ile Ser His Pro Asp Met Val Asp Phe Ala Arg Gly Lys Thr Phe Phe
          225          230          235

ggg gcc gtg atg gtg ggg tga gggaatatga gtgcgtggtg cgagtgcgtg  773
Gly Ala Val Met Val Gly *
          240

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aatattgggg gcccgacgc ccaggacccc atggcagtg gaaaaatgta ggagactggt 833

SEQLIST.TXT

tggaaattga ttttgaacct gatgaaaata aagaatggaa agcttcagtg ctgccgataa 893
a 894

<210> 13
<211> 327
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(327)
<223> FKBP1A open reading frame for FK506 Binding
Protein 1A (macrophilin 12) mRNA coding region

<400> 13
atg gga gtg cag gtg gaa acc atc tcc cca gga gac ggg cgc acc ttc 48
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15
ccc aag cgc ggc cag acc tgc gtg gtg cac tac acc ggg atg ctt gaa 96
Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30
gat gga aag aaa ttt gat tcc tcc cgg gac aga aac aag ccc ttt aag 144
Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45
ttt atg cta ggc aag cag gag gtg atc cga ggc tgg gaa gaa ggg gtt 192
Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60
gcc cag atg agt gtg ggt cag aga gcc aaa ctg act ata tct cca gat 240
Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80
tat gcc tat ggt gcc act ggg cac cca ggc atc atc cca cca cat gcc 288
Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95
act ctc gtc ttc gat gtg gag ctt cta aaa ctg gaa tga 327
Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu *
100 105

<210> 14
<211> 21
<212> DNA
<213> Homo sapiens

<220>
<221> primer_bind
<222> (1)...(21)
<223> Amplification primer for human LTA - forward

<400> 14
acaccactg aacgtctctt c 21

<210> 15
<211> 21
<212> DNA
<213> Homo sapiens

<220>
<221> primer_bind
<222> (1)...(21)
<223> Amplification primer for human LTA - reverse

<400> 15

SEQLIST.TXT

tctcaatccc tgaggaagtg g 21

<210> 16
 <211> 24
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer_bind
 <222> (1)...(24)
 <223> Sequencing primer for human LTA - forward

<400> 16
 tcagccaaac cttgagccct agag 24

<210> 17
 <211> 34
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer_bind
 <222> (1)...(34)
 <223> Sequencing primer for human LTA - reverse

<400> 17
 atgtttacca atgaggtgag cagcaggttt gcgg 34

<210> 18
 <211> 20
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer_bind
 <222> (1)...(20)
 <223> Amplification primer for human TNF - forward

<400> 18
 tgggagtgag aacttcccag 20

<210> 19
 <211> 20
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer_bind
 <222> (1)...(20)
 <223> Amplification primer for human TNF - reverse

<400> 19
 tgagctcatc tggaggaagc 20

<210> 20
 <211> 20
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer_bind
 <222> (1)...(20)
 <223> Sequencing primer for human TNF - forward

<400> 20
 tgggagtgag aacttcccag 20

<210> 21

SEQLIST.TXT

<211> 20
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer_bind
 <222> (1)...(20)
 <223> Sequencing primer for human TNF - reverse

<400> 21
 cttaaacgtc ccctgtattc

20

<210> 22
 <211> 894
 <212> DNA
 <213> Homo sapiens

<220>
 <221> variation
 <222> (9)...(743)
 <223> LTB*1 (G) polymorphism coding region

<400> 22
 cagtctcaat gggggcactg gggctggagg gcaggggtgg gaggctccag gggaggggtt 60
 ccctcctgct agctgtggca ggagccactt ctctggtgac cttgttgctg gcggtgccta 120
 tcactgtcct ggctgtgctg gccttagtgcc cccaggatca gggaggactg gtaacggaga 180
 cggccgaccc cggggcacag gcccagcaag gactgggggtt tcagaagctg ccagaggagg 240
 agccagaaac agatctcagc cccgggctcc cagctgcccc cctcataggc gctccgctga 300
 aggggcaggg gctaggctgg gagacgacga aggaacaggc gtttctgacg agcgggacgc 360
 agttctcgga cgccgagggg ctggcgctcc cgaggacgg cctctattac ctctactgtc 420
 tcgtcggcta ccggggccgg gcgccccctg gcggcgggga ccccagggc cgctcgggtca 480
 cgctgcgcag ctctctgtac cgggcggggg gcgcctacgg gccgggact cccgagctgc 540
 tgctcgaggg cgccgagacg gtgactccag tgctggaccc ggccaggaga caagggtacg 600
 ggcctctctg gtacacgagc gtgggggttcg gcggcctggt gcagctccgg aggggcgaga 660
 ggggtgtacgt caacatcagt caccctcgata tgggtggactt cgcgagaggg aagaccttct 720
 ttggggccgt gatggtgggg tgaggggaata tgagtgcgtg gtgcgagtgc gtgaatattg 780
 ggggcccggg cgcccaggac cccatggcag tgggaaaaat gtaggagact gtttggaaat 840
 tgattttgaa cctgatgaaa ataaagaatg gaaagcttca gtgctgccga taaa 894